

=====

Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Keisha Douglas

Timestamp: [year=2008; month=12; day=1; hr=11; min=44; sec=45; ms=962;]

=====

Application No: 10510628 Version No: 3.0

Input Set:

Output Set:

Started: 2008-11-06 15:38:29.253
Finished: 2008-11-06 15:38:33.491
Elapsed: 0 hr(s) 0 min(s) 4 sec(s) 238 ms
Total Warnings: 7
Total Errors: 0
No. of SeqIDs Defined: 11
Actual SeqID Count: 11

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)

SEQUENCE LISTING

```

<110>  HEGEMANN, Peter

<120>  USE OF BIOLOGICAL PHOTORECEPTORS AS DIRECTLY LIGHT-ACTIVATED ION
      CHANNELS

<130>  231181

<140>  10510628
<141>  2005-05-09

<150>  PCT/EP03/03799
<151>  2003-04-11

<150>  102 16 005.8
<151>  2002-04-11

<160>  11

<170>  PatentIn version 3.5

<210>  1
<211>  712
<212>  PRT
<213>  Chlamydomonas reinhardtii

<220>
<221>  MISC_FEATURE
<222>  (1)..(712)
<223>  Amino acid sequence of CHOP-1 from Chlamydomonas reinhardtii

<400>  1

Met Ser Arg Arg Pro Trp Leu Leu Ala Leu Ala Leu Ala Val Ala Leu
1          5          10          15

Ala Ala Gly Ser Ala Gly Ala Ser Thr Gly Ser Asp Ala Thr Val Pro
          20          25          30

Val Ala Thr Gln Asp Gly Pro Asp Tyr Val Phe His Arg Ala His Glu
          35          40          45

Arg Met Leu Phe Gln Thr Ser Tyr Thr Leu Glu Asn Asn Gly Ser Val
          50          55          60

Ile Cys Ile Pro Asn Asn Gly Gln Cys Phe Cys Leu Ala Trp Leu Lys
65          70          75          80

Ser Asn Gly Thr Asn Ala Glu Lys Leu Ala Ala Asn Ile Leu Gln Trp

```

85

90

95

Ile Thr Phe Ala Leu Ser Ala Leu Cys Leu Met Phe Tyr Gly Tyr Gln
 100 105 110

Thr Trp Lys Ser Thr Cys Gly Trp Glu Glu Ile Tyr Val Ala Thr Ile
 115 120 125

Glu Met Ile Lys Phe Ile Ile Glu Tyr Phe His Glu Phe Asp Glu Pro
 130 135 140

Ala Val Ile Tyr Ser Ser Asn Gly Asn Lys Thr Val Trp Leu Arg Tyr
 145 150 155 160

Ala Glu Trp Leu Leu Thr Cys Pro Val Ile Leu Ile His Leu Ser Asn
 165 170 175

Leu Thr Gly Leu Ala Asn Asp Tyr Asn Lys Arg Thr Met Gly Leu Leu
 180 185 190

Val Ser Asp Ile Gly Thr Ile Val Trp Gly Thr Thr Ala Ala Leu Ser
 195 200 205

Lys Gly Tyr Val Arg Val Ile Phe Phe Leu Met Gly Leu Cys Tyr Gly
 210 215 220

Ile Tyr Thr Phe Phe Asn Ala Ala Lys Val Tyr Ile Glu Ala Tyr His
 225 230 235 240

Thr Val Pro Lys Gly Ile Cys Arg Asp Leu Val Arg Tyr Leu Ala Trp
 245 250 255

Leu Tyr Phe Cys Ser Trp Ala Met Phe Pro Val Leu Phe Leu Leu Gly
 260 265 270

Pro Glu Gly Phe Gly His Ile Asn Gln Phe Asn Ser Ala Ile Ala His
 275 280 285

Ala Ile Leu Asp Leu Ala Ser Lys Asn Ala Trp Ser Met Met Gly His
 290 295 300

Phe Leu Arg Val Lys Ile His Glu His Ile Leu Leu Tyr Gly Asp Ile
 305 310 315 320

Arg Lys Lys Gln Lys Val Asn Val Ala Gly Gln Glu Met Glu Val Glu
325 330 335

Thr Met Val His Glu Glu Asp Asp Glu Thr Gln Lys Val Pro Thr Ala
340 345 350

Lys Tyr Ala Asn Arg Asp Ser Phe Ile Ile Met Arg Asp Arg Leu Lys
355 360 365

Glu Lys Gly Phe Glu Thr Arg Ala Ser Leu Asp Gly Asp Pro Asn Gly
370 375 380

Asp Ala Glu Ala Asn Ala Ala Ala Gly Gly Lys Pro Gly Met Glu Met
385 390 395 400

Gly Lys Met Thr Gly Met Gly Met Gly Met Gly Ala Gly Met Gly Met
405 410 415

Ala Thr Ile Asp Ser Gly Arg Val Ile Leu Ala Val Pro Asp Ile Ser
420 425 430

Met Val Asp Phe Phe Arg Glu Gln Phe Ala Arg Leu Pro Val Pro Tyr
435 440 445

Glu Leu Val Pro Ala Leu Gly Ala Glu Asn Thr Leu Gln Leu Val Gln
450 455 460

Gln Ala Gln Ser Leu Gly Gly Cys Asp Phe Val Leu Met His Pro Glu
465 470 475 480

Phe Leu Arg Asp Arg Ser Pro Thr Gly Leu Leu Pro Arg Leu Lys Met
485 490 495

Gly Gly Gln Arg Ala Ala Ala Phe Gly Trp Ala Ala Ile Gly Pro Met
500 505 510

Arg Asp Leu Ile Glu Gly Ser Gly Val Asp Gly Trp Leu Glu Gly Pro
515 520 525

Ser Phe Gly Ala Gly Ile Asn Gln Gln Ala Leu Val Ala Leu Ile Asn
530 535 540

Arg Met Gln Gln Ala Lys Lys Met Gly Met Met Gly Gly Met Gly Met
545 550 555 560

Gly Met Gly Gly Gly Met Gly Met Gly Met Gly Met Gly Met Gly Met
565 570 575

Ala Pro Ser Met Asn Ala Gly Met Thr Gly Gly Met Gly Gly Ala Ser
580 585 590

Met Gly Gly Ala Val Met Gly Met Gly Met Gly Met Gln Pro Met Gln
595 600 605

Gln Ala Met Pro Ala Met Ser Pro Met Met Thr Gln Gln Pro Ser Met
610 615 620

Met Ser Gln Pro Ser Ala Met Ser Ala Gly Gly Ala Met Gln Ala Met
625 630 635 640

Gly Gly Val Met Pro Ser Pro Ala Pro Gly Gly Arg Val Gly Thr Asn
645 650 655

Pro Leu Phe Gly Ser Ala Pro Ser Pro Leu Ser Ser Gln Pro Gly Ile
660 665 670

Ser Pro Gly Met Ala Thr Pro Pro Ala Ala Thr Ala Ala Pro Ala Ala
675 680 685

Gly Gly Ser Glu Ala Glu Met Leu Gln Gln Leu Met Ser Glu Ile Asn
690 695 700

Arg Leu Lys Asn Glu Leu Gly Glu
705 710

<210> 2
<211> 737
<212> PRT
<213> Chlamydomonas reinhardtii

<220>
<221> MISC_FEATURE
<222> (1)..(737)
<223> Amino acid sequence of CHOP-2 from Chlamydomonas reinhardtii

<220>

<221> MISC_FEATURE
<222> (2)..(737)
<223> Amino acid sequence of CHOP-2 from Chlamydomonas reinhardtii

<400> 2

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe
1 5 10 15

Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp
20 25 30

Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala
35 40 45

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile
50 55 60

Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly
65 70 75 80

Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu
85 90 95

Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr
100 105 110

Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys
115 120 125

Pro Val Ile Leu Ile His Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp
130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile
145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile
165 170 175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala
180 185 190

Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys
195 200 205

Arg	Gln	Val	Val	Thr	Gly	Met	Ala	Trp	Leu	Phe	Phe	Val	Ser	Trp	Gly	210	215	220	
Met	Phe	Pro	Ile	Leu	Phe	Ile	Leu	Gly	Pro	Glu	Gly	Phe	Gly	Val	Leu	225	230	235	240
Ser	Val	Tyr	Gly	Ser	Thr	Val	Gly	His	Thr	Ile	Ile	Asp	Leu	Met	Ser	245	250	255	
Lys	Asn	Cys	Trp	Gly	Leu	Leu	Gly	His	Tyr	Leu	Arg	Val	Leu	Ile	His	260	265	270	
Glu	His	Ile	Leu	Ile	His	Gly	Asp	Ile	Arg	Lys	Thr	Thr	Lys	Leu	Asn	275	280	285	
Ile	Gly	Gly	Thr	Glu	Ile	Glu	Val	Glu	Thr	Leu	Val	Glu	Asp	Glu	Ala	290	295	300	
Glu	Ala	Gly	Ala	Val	Asn	Lys	Gly	Thr	Gly	Lys	Tyr	Ala	Ser	Arg	Glu	305	310	315	320
Ser	Phe	Leu	Val	Met	Arg	Asp	Lys	Met	Lys	Glu	Lys	Gly	Ile	Asp	Val	325	330	335	
Arg	Ala	Ser	Leu	Asp	Asn	Ser	Lys	Glu	Val	Glu	Gln	Glu	Gln	Ala	Ala	340	345	350	
Arg	Ala	Ala	Met	Met	Met	Met	Asn	Gly	Asn	Gly	Met	Gly	Met	Gly	Met	355	360	365	
Gly	Met	Asn	Gly	Met	Asn	Gly	Met	Gly	Gly	Met	Asn	Gly	Met	Ala	Gly	370	375	380	
Gly	Ala	Lys	Pro	Gly	Leu	Glu	Leu	Thr	Pro	Gln	Leu	Gln	Pro	Gly	Arg	385	390	395	400
Val	Ile	Leu	Ala	Val	Pro	Asp	Ile	Ser	Met	Val	Asp	Phe	Phe	Arg	Glu	405	410	415	
Gln	Phe	Ala	Gln	Leu	Ser	Val	Thr	Tyr	Glu	Leu	Val	Pro	Ala	Leu	Gly	420	425	430	

Ala Asp Asn Thr Leu Ala Leu Val Thr Gln Ala Gln Asn Leu Gly Gly
435 440 445

Val Asp Phe Val Leu Ile His Pro Glu Phe Leu Arg Asp Arg Ser Ser
450 455 460

Thr Ser Ile Leu Ser Arg Leu Arg Gly Ala Gly Gln Arg Val Ala Ala
465 470 475 480

Phe Gly Trp Ala Gln Leu Gly Pro Met Arg Asp Leu Ile Glu Ser Ala
485 490 495

Asn Leu Asp Gly Trp Leu Glu Gly Pro Ser Phe Gly Gln Gly Ile Leu
500 505 510

Pro Ala His Ile Val Ala Leu Val Ala Lys Met Gln Gln Met Arg Lys
515 520 525

Met Gln Gln Met Gln Gln Ile Gly Met Met Thr Gly Gly Met Asn Gly
530 535 540

Met Gly Gly Gly Met Gly Gly Gly Met Asn Gly Met Gly Gly Gly Asn
545 550 555 560

Gly Met Asn Asn Met Gly Asn Gly Met Gly Gly Gly Met Gly Asn Gly
565 570 575

Met Gly Gly Asn Gly Met Asn Gly Met Gly Gly Gly Asn Gly Met Asn
580 585 590

Asn Met Gly Gly Asn Gly Met Ala Gly Asn Gly Met Gly Gly Gly Met
595 600 605

Gly Gly Asn Gly Met Gly Gly Ser Met Asn Gly Met Ser Ser Gly Val
610 615 620

Val Ala Asn Val Thr Pro Ser Ala Ala Gly Gly Met Gly Gly Met Met
625 630 635 640

Asn Gly Gly Met Ala Ala Pro Gln Ser Pro Gly Met Asn Gly Gly Arg
645 650 655

Leu Gly Thr Asn Pro Leu Phe Asn Ala Ala Pro Ser Pro Leu Ser Ser

660

665

670

Gln Leu Gly Ala Glu Ala Gly Met Gly Ser Met Gly Gly Met Gly Gly
675 680 685

Met Ser Gly Met Gly Gly Met Gly Gly Met Gly Gly Met Gly Gly Ala
690 695 700

Gly Ala Ala Thr Thr Gln Ala Ala Gly Gly Asn Ala Glu Ala Glu Met
705 710 715 720

Leu Gln Asn Leu Met Asn Glu Ile Asn Arg Leu Lys Arg Glu Leu Gly
725 730 735

Glu

<210> 3

<211> 259

<212> PRT

<213> Halobacterium salinarum

<220>

<221> MISC_FEATURE

<222> (1)..(259)

<223> Amino acid sequence of bacteriorhodopsin from Halobacterium
salinarum

<400> 3

Met Leu Pro Thr Ala Val Glu Gly Val Ser Gln Ala Gln Ile Thr Gly
1 5 10 15

Arg Pro Glu Trp Ile Trp Leu Ala Leu Gly Thr Ala Leu Met Gly Leu
20 25 30

Gly Thr Leu Tyr Phe Leu Val Lys Gly Met Gly Val Ser Asp Pro Asp
35 40 45

Ala Lys Lys Phe Tyr Ala Ile Thr Thr Leu Val Pro Ala Ile Ala Phe
50 55 60

Thr Met Tyr Leu Ser Met Leu Leu Gly Tyr Gly Leu Thr Met Val Pro
65 70 75 80

Phe Gly Gly Glu Gln Asn Pro Ile Tyr Trp Ala Arg Tyr Ala Asp Trp
 85 90 95

Leu Phe Thr Thr Pro Leu Leu Leu Leu Asp Leu Ala Leu Leu Val Asp
 100 105 110

Ala Asp Gln Gly Thr Ile Leu Ala Leu Val Gly Ala Asp Gly Ile Met
 115 120 125

Ile Gly Thr Gly Leu Val Gly Ala Leu Thr Lys Val Tyr Ser Tyr Arg
 130 135 140

Phe Val Trp Trp Ala Ile Ser Thr Ala Ala Met Leu Tyr Ile Leu Tyr
 145 150 155 160

Val Leu Phe Phe Gly Phe Thr Ser Lys Ala Glu Ser Met Arg Pro Glu
 165 170 175

Val Ala Ser Thr Phe Lys Val Leu Arg Asn Val Thr Val Val Leu Trp
 180 185 190

Ser Ala Tyr Pro Val Val Trp Leu Ile Gly Ser Glu Gly Ala Gly Ile
 195 200 205

Val Pro Leu Asn Ile Glu Thr Leu Leu Phe Met Val Leu Asp Val Ser
 210 215 220

Ala Lys Val Gly Phe Gly Leu Ile Leu Leu Arg Ser Arg Ala Ile Phe
 225 230 235 240

Gly Glu Ala Glu Ala Pro Glu Pro Ser Ala Gly Asp Gly Ala Ala Ala
 245 250 255

Thr Ser Asp

<210> 4
 <211> 315
 <212> PRT
 <213> Chlamydomonas reinhardtii

<220>
 <221> MISC_FEATURE
 <222> (1)..(315)

<223> Amino acid sequence of the CHOP2-315/H134R mutant

<400> 4

Met Asp Tyr Gly Gly Ala Leu Ser Ala Val Gly Arg Glu Leu Leu Phe
1 5 10 15

Val Thr Asn Pro Val Val Val Asn Gly Ser Val Leu Val Pro Glu Asp
20 25 30

Gln Cys Tyr Cys Ala Gly Trp Ile Glu Ser Arg Gly Thr Asn Gly Ala
35 40 45

Gln Thr Ala Ser Asn Val Leu Gln Trp Leu Ala Ala Gly Phe Ser Ile
50 55 60

Leu Leu Leu Met Phe Tyr Ala Tyr Gln Thr Trp Lys Ser Thr Cys Gly
65 70 75 80

Trp Glu Glu Ile Tyr Val Cys Ala Ile Glu Met Val Lys Val Ile Leu
85 90 95

Glu Phe Phe Phe Glu Phe Lys Asn Pro Ser Met Leu Tyr Leu Ala Thr
100 105 110

Gly His Arg Val Gln Trp Leu Arg Tyr Ala Glu Trp Leu Leu Thr Cys
115 120 125

Pro Val Ile Leu Ile Arg Leu Ser Asn Leu Thr Gly Leu Ser Asn Asp
130 135 140

Tyr Ser Arg Arg Thr Met Gly Leu Leu Val Ser Asp Ile Gly Thr Ile
145 150 155 160

Val Trp Gly Ala Thr Ser Ala Met Ala Thr Gly Tyr Val Lys Val Ile
165 170 175

Phe Phe Cys Leu Gly Leu Cys Tyr Gly Ala Asn Thr Phe Phe His Ala
180 185 190

Ala Lys Ala Tyr Ile Glu Gly Tyr His Thr Val Pro Lys Gly Arg Cys
195 200 205

Arg Gln Val Val Thr Gly Met Ala Trp Leu Phe Phe Val Ser Trp Gly

210

215

220

Met Phe Pro Ile Leu Phe Ile Leu Gly P